

032301.1171.seq.ST25.txt
SEQUENCE LISTING

<110> NAMPOOTHIRI, Madhavan
<120> Nucleotide Sequences Coding for the CdsA Gene
<130> 032301 WD 1171
<140> 09/853,641
<141> 2001-05-14
<160> 4
<170> PatentIn version 3.1
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gcaagagtgt ttggaagaat tttttcgaaa atgctggcac catcaacagt gacattgtta 180
gaaacttcaa ggagaaccc atg aat gaa cgg gag caa cat cac cgg tcc atg 232
Met Asn Glu Pro Glu Gln His His Arg Ser Met
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agg atg ccc aaa ccc aaa aat aat gcg ggt cga gat ctc aaa gct gcc 280
Arg Met Pro Lys Pro Lys Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala
15 20 25
att gct gtg ggg atc gga ctg ggg gtc ctg gtt ctt ttg ggg att gtc 328
Ile Ala Val Gly Ile Gly Leu Gly Val Leu Val Leu Leu Gly Ile Val
30 35 40
cta agc cca tgg ggt tgg tac atc ctc gtt gca ggt ttt atg gct gca 376
Leu Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala
45 50 55
gca aca tgg gaa gtt ggt agc aga ctt aaa gaa ggc ggc tat cat ttg 424
Ala Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu
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032301.1171.seq.ST25.txt

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Pro Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser	
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tggt cca ttt ggc acg atg ggc att ttg gcg tct ttt gtg gcc act gtg	520
Trp Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val	
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ttg gtg ctg atg tat ttc cga att ttc tac aat ggc acg gaa aaa gaa	568
Leu Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu	
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gcc cgc aac tat ttg agg gac acc tct gtg ggc atc ttc gtg ctc acc	616
Ala Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr	
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Trp Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln	
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aac aat tcc atc ccg ggt aca tat ttc att ttg acg ttc atg ctg tgt	712
Asn Asn Ser Ile Pro Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys	
160 165 170	
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Val Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly	
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Ser His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly	
190 195 200	
ttt gcc ggc tcc att gtc tta gga tcg gtc act ggt gca ctc agt gtt	856
Phe Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val	
205 210 215	
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His Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys	
220 225 230 235	
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Lys Arg Asp Leu Gly Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His	
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Gly Gly Leu Met Asp Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val	
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Thr Trp Leu Ile Leu Ser Val Ile Ser Ser Ser Tyr Pro Ser	
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032301.1171.seq.ST25.txt

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35 40 45

Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val
50 55 60

Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro Leu Pro Ile Met
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Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp Pro Phe Gly Thr
85 90 95

Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr
100 105 110

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115 120 125

Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe
130 135 140

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145 150 155 160

Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp
165 170 175

Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala
180 185 190

032301.1171.seq.ST25.txt

Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile
195 200 205

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210 215 220

His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys
225 230 235 240

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245 250 255

Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp
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Ser Val Ile Ser Ser Ser Tyr Pro Ser
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